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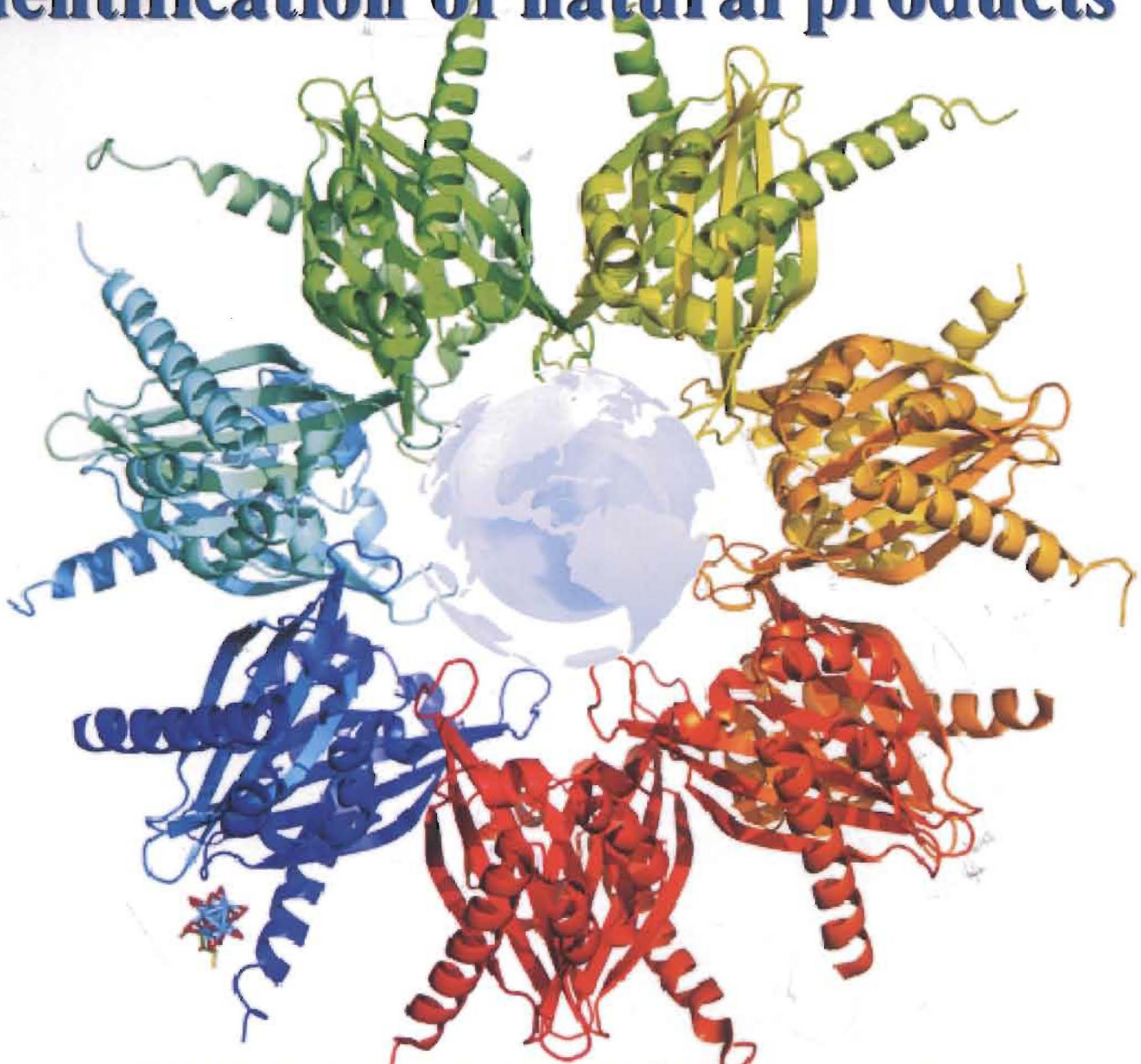

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Genome mining indicates that the genus *Xanthomonas* is a promising reservoir for new bioactive non-ribosomally synthesized peptides

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Introduction

Xanthomonas is a large genus of Gram-negative bacteria that cause disease in hundreds of plant species. To date, the only known small molecule synthesized by non-ribosomal peptide synthesis (NRPS) in this genus is albicidin produced by *Xanthomonas albilineans* [1]. The DNA gyrase inhibitor albicidin is not only an important virulence factor but also a possible lead structure for novel antibiotics [2]. This study aims to estimate the biosynthetic potential of *Xanthomonas* spp. by *in silico* analyses of NRPS genes with unknown function recently identified in the sequenced genomes of *X. albilineans* and related species of *Xanthomonas*.

Experimental

In silico analyses were performed on NRPS genes present in the published finished genome sequence of *X. albilineans* strain GPE PC73 (accession n°: NC_013722.1), in the published draft genome sequence of *Xanthomonas oryzae* pv. *oryzae* strain X11-5A (accession n°: AFHK00000000.1), in the unpublished sequence of the 82-kb length region containing META-B in *X. oryzae* pv. *oryzae* strain BAI-3 and in the unpublished draft genome sequence of strain *Xanthomonas* spp. XaS3. Specificity of adenylation domains in NRPS and signatures were predicted using the web server NRPSpredictor2 [3].

Results and discussion

This study revealed four strains of the genus *Xanthomonas* possessing a novel homologous NRPS gene cluster, hereafter referred to as META-B. The sequence alignment of META-B gene clusters from *Xanthomonas* strains is indicative of the biosynthesis of lipopeptides or peptides linked to an other non-amino acid substrate, and involving the biosynthesis and incorporation of the non-proteinogenic amino acids Dpg (3,5-dihydroxyphenyl-glycine), Dab (2,4-diamino butyric acid), β-Hty (β-hydroxy-tyrosine) as well as of amino acid(s) of unknown identity (Figure 1; [4]). This study revealed that each sequence of the peptide is strain-specific. If the biosynthetic pathways are functional, these peptides may exert different biological functions in plant-bacteria interactions.

Conclusions

This extensive *in silico* study shows that the genus *Xanthomonas* constitutes a promising reservoir for new non-ribosomally synthesized peptides. Experimental elucidation of this

promising biosynthetic potential should contribute to the study of plant-bacteria interaction and also to the drug discovery.

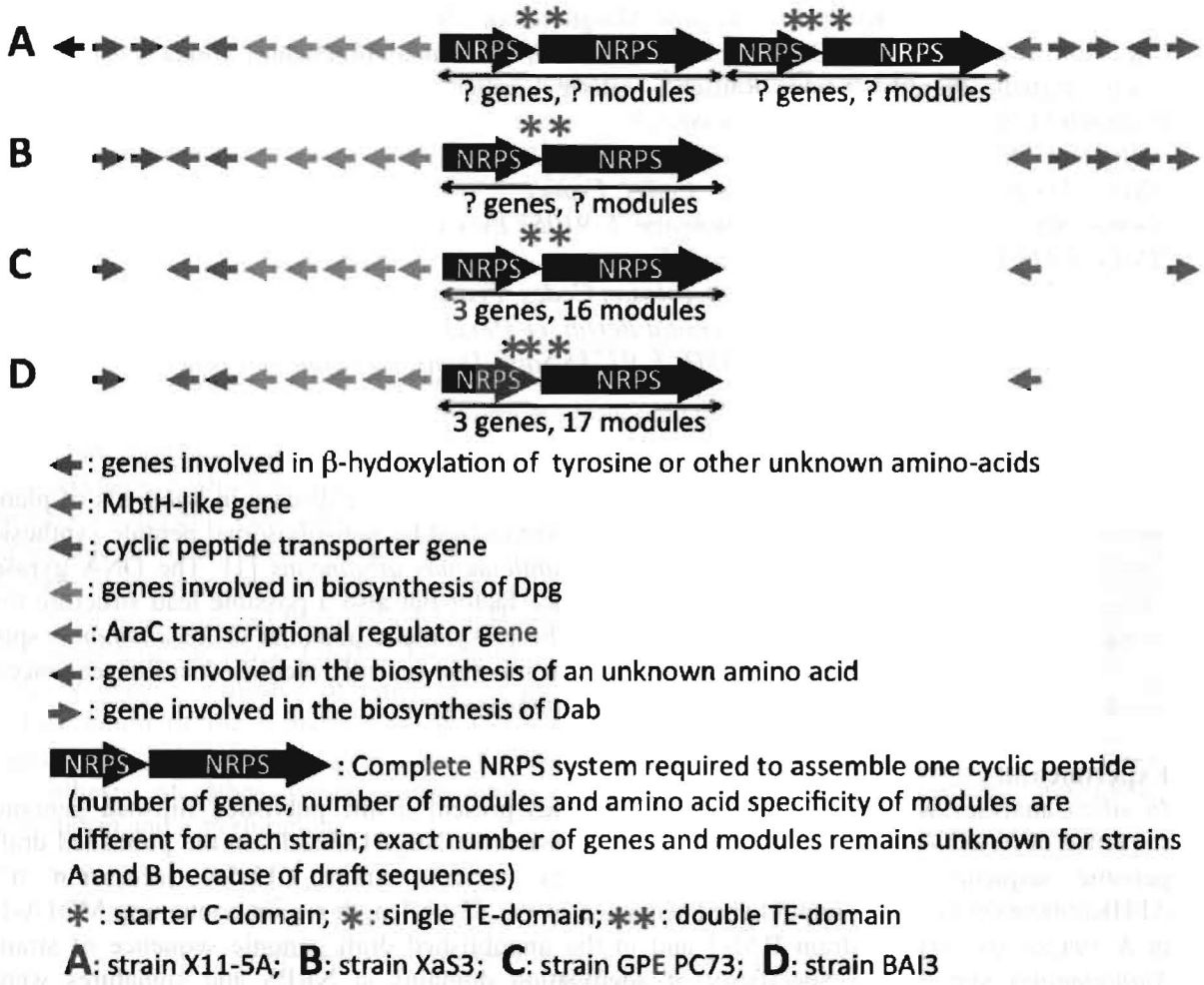

Figure 1. Schematic representation of the META-B gene cluster in four strains of *Xanthomonas*

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